

## SEQUENCE LISTING

<110> Gilbert, Teresa  
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<120> GROWTH FACTOR HOMOLOG ZVEGF4

<130> 99-19

<150> US 60/132,250

<151> 1999-05-03

<150> US 60/164,463

<151> 1999-11-10

<150> US 60/180,169

<151> 2000-02-04

<160> 53

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1882

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (226)...(1338)

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cagggcgagc gcaggcggcg agagcgcagg gcggcgcggc gtcggtcccg ggagcagaac	180
ccggcttttt cttggagcga cgctgtctct agtcgctgat cccaa atg cac cgg ctc	237
Met His Arg Leu	

atc ttt gtc tac act cta atc tgc gca aac ttt tgc agc tgt cgg gac Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys Ser Cys Arg Asp 5 10 15 20	285
act tct gca acc ccg cag agc gca tcc atc aaa gct ttg cgc aac gcc Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala Leu Arg Asn Ala 25 30 35	333
aac ctc agg cga gat gag agc aat cac ctc aca gac ttg tac cga aga Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Arg Arg 40 45 50	381
gat gag acc atc cag gtg aaa gga aac ggc tac gtg cag agt cct aga Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln Ser Pro Arg 55 60 65	429
ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca tgg cgg ctt cac Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Arg Leu His 70 75 80	477
tct cag gag aat aca cgg ata cag cta gtg ttt gac aat cag ttt gga Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn Gln Phe Gly 85 90 95 100	525
tta gag gaa gca gaa aat gat atc tgt agg tat gat ttt gtg gaa gtt Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val 105 110 115	573
gaa gat ata tcc gaa acc agt acc att att aga gga cga tgg tgt gga Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly 120 125 130	621
cac aag gaa gtt cct cca agg ata aaa tca aga acg aac caa att aaa His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys 135 140 145	669
atc aca ttc aag tcc gat gac tac ttt gtg gct aaa cct gga ttc aag Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys 150 155 160	717
att tat tat tct ttg ctg gaa gat ttc caa ccc gca gca gct tca gag Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala Ala Ala Ser Glu 165 170 175 180	765

acc aac tgg gaa tct gtc aca agc tct att tca ggg gta tcc tat aac Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly Val Ser Tyr Asn 185 190 195	813
tct cca tca gta acg gat ccc act ctg att gcg gat gct ctg gac aaa Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys 200 205 210	861
aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc aag tac ttc aat Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn 215 220 225	909
cca gag tca tgg caa gaa gat ctt gag aat atg tat ctg gac acc cct Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro 230 235 240	957
cgg tat cga ggc agg tca tac cat gac cgg aag tca aaa gtt gac ctg Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu 245 250 255 260	1005
gat agg ctc aat gat gat gcc aag cgt tac agt tgc act ccc agg aat Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn 265 270 275	1053
tac tcg gtc aat ata aga gaa gag ctg aag ttg gcc aat gtg gtc ttc Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala Asn Val Val Phe 280 285 290	1101
ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga aat tgt ggc tgt Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys 295 300 305	1149
gga act gtc aac tgg agg tcc tgc aca tgc aat tca ggg aaa acc gtg Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser Gly Lys Thr Val 310 315 320	1197
aaa aag tat cat gag gta tta cag ttt gag cct ggc cac atc aag agg Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly His Ile Lys Arg 325 330 335 340	1245

agg ggt aga gct aag acc atg gct cta gtt gac atc cag ttg gat cac 1293  
 Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile Gln Leu Asp His  
 345 350 355

cat gaa cga tgc gat tgt atc tgc agc tca aga cca cct cga taa 1338  
 His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg \*  
 360 365 370

gagaatgtgc acatccttac attaagcctg aaagaacctt tagtttaagg aggggtgagat 1398  
 aagagaccct tttctacca gcaaccaaac ttactactag cctgcaatgc aatgaacaca 1458  
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<211> 370

<212> PRT

<213> Homo sapiens

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 1 5 10 15  
 Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala  
 20 25 30  
 Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp  
 35 40 45  
 Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val  
 50 55 60  
 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr  
 65 70 75 80  
 Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp  
 85 90 95  
 Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp  
 100 105 110  
 Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly  
 115 120 125  
 Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr  
 130 135 140

Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys  
 145 150 155 160  
 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala  
 165 170 175  
 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly  
 180 185 190  
 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp  
 195 200 205  
 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu  
 210 215 220  
 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr  
 225 230 235 240  
 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser  
 245 250 255  
 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys  
 260 265 270  
 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala  
 275 280 285  
 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly  
 290 295 300  
 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser  
 305 310 315 320  
 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly  
 325 330 335  
 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile  
 340 345 350  
 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro  
 355 360 365  
 Pro Arg  
 370

<210> 3

<211> 126

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<213> Artificial Sequence

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<223> polypeptide motif

<221> VARIANT

<222> (2)...(19)

<223> Xaa = Any Amino Acid

<221> VARIANT  
 <222> (20)...(34)  
 <223> Xaa = Any Amino Acid or is not present

<221> VARIANT  
 <222> (36)...(45)  
 <223> Xaa = Any Amino Acid

<221> VARIANT  
 <222> (46)...(72)  
 <223> Xaa = Any Amino Acid or is not present

<221> VARIANT  
 <222> (74)...(93)  
 <223> Xaa = Any Amino Acid

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 <223> Xaa = Any Amino Acid or is not present

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 <223> Xaa = Any Amino Acid

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Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1			5					10							15	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25						30		
Xaa	Xaa	Cys	Xaa	Gly	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		35				40						45				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		50				55					60					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65				70					75						80	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			85					90						95		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			100					105						110		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Cys		
		115						120								

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<221> VARIANT  
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 <223> Xaa = Lys or Arg

<221> VARIANT  
 <222> (4)...(4)  
 <223> Xaa = Asp, Asn or Glu

<221> VARIANT  
 <222> (5)...(5)  
 <223> Xaa = Trp, Tyr or Phe

<221> VARIANT  
 <222> (6)...(16)  
 <223> Xaa = Any Amino Acid

<221> VARIANT  
 <222> (17)...(20)  
 <223> Xaa = Any Amino Acid or is not present

<221> VARIANT  
 <222> (22)...(22)  
 <223> Xaa = Lys or Arg

<221> VARIANT  
 <222> (23)...(23)  
 <223> Xaa = Trp, Tyr or Phe

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 Cys Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 1 5 10 15  
 Xaa Xaa Xaa Xaa Gly Xaa Xaa Cys  
 20

<210> 5  
 <211> 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; polypeptide tag

&lt;400&gt; 5

Glu Tyr Met Pro Met Glu

1

5

&lt;210&gt; 6

&lt;211&gt; 1110

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; degenerate sequence

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1110)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 6

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acnwsngcna	cncncarws	ngcnwsnath	aargcnytnm	gnaaygcnaa	yytnmngmgn	120
gaygarwsna	aycaytnac	ngayytnay	mgnmngayg	aracnathca	rgtnaaragn	180
aayggntayg	tncarwsncc	nmngnttyccn	aaywsntayc	cnmgnaayyt	nytnytnacn	240
tggmgnytn	aywsncarga	raayacnmgn	athcarytng	tnattygayaa	ycarttygg	300
ytngargarg	cngaraayga	yathtgymgn	taygayttg	tngargtnga	rgayathwsn	360
garacnwsna	cnathathmg	ngnmngntgg	tgygncaya	argargtncc	nccnmgnath	420
aarwsnmgna	cnaaycarat	haarathacn	ttyaarwsng	aygaytaytt	ygtngcnaar	480
ccnggnttga	arathtayta	ywsnytnytn	gargayttyc	arccngcngc	ngcnwsngar	540
acnaaytggg	arwsngtnac	nwsnwsnath	wsngngntnw	sntayaayws	nccnwsngtn	600
acngayccna	cnytnathgc	ngaygcnytn	gayaaraara	thgcngartt	ygayacngtn	660
gargayytny	tnaartaytt	yaayccngar	wsntggcarg	argayytnga	raayatgtay	720
ytngayacnc	cnmgntaymg	ngnmgnwsn	taycaygaym	gnaarwsnaa	rgtngayytn	780
gaymgnytna	aygaygaygc	naarmgntay	wsntgyacnc	cnmgnaayta	ywsngtnaay	840
athmgngarg	arytnaaryt	ngcnaaygt	gtnttyttyc	cnmgntgyyt	nytngtncar	900
mgntgyggng	gnaaytgygg	ntgyggnacn	gtnaaytggm	gnwsntgyac	ntgyaaywsn	960
ggnaaracng	tnaaraarta	ycaygargtn	ytncarttyg	arccngngca	yathaarmgn	1020
mgnggmngng	cnaaracnat	ggcnytngt	gayathcary	tngaycayca	ygarmgntgy	1080
gaytgyatht	gywsnwsnmg	nccnccnmgn				1110



<210> 7  
 <211> 17  
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 <213> Artificial Sequence

<220>  
 <223> oligonucleotide primer

<221> misc\_feature  
 <222> (1)...(17)  
 <223> n = A,T,C or G

<400> 7  
 mgntgyggng gnaaytg 17

<210> 8  
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<400> 8  
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<210> 9  
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<221> misc\_feature  
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 <223> n = A,T,C or G

<400> 9

carywncns hrcanck 17

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<221> misc\_feature  
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 <223> n = A,T,C or G

<400> 10  
 ttyttyccnm gntgyt 17

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<400> 11  
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<400> 12  
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 <210> 13  
 <211> 17  
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 <222> (1)...(17)  
 <223> n = A,T,C or G  
  
 <400> 13  
 caygarmgnt gygaytg 17  
  
 <210> 14  
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 <210> 15  
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<222> (1)...(17)

<223> n = A,T,C or G

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17

<210> 16

<211> 17

<212> DNA

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<221> misc\_feature

<222> (1)...(17)

<223> n = A,T,C or G

<400> 16

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17

<210> 17

<211> 17

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide primer

<221> misc\_feature

<222> (1)...(17)

<223> n = A,T,C or G

<400> 17

tgyhnnmcm knrmdh

17

<210> 18

<211> 17

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide primer

<221> misc\_feature  
 <222> (1)...(17)  
 <223> n = A,T,C or G

<400> 18  
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<210> 19  
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<221> misc\_feature  
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 <223> n = A,T,C or G

<400> 19  
 ntaygaytby gtngargt 18

<210> 20  
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<400> 20  
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<210> 21  
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 <222> (1)...(18)  
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 <400> 21  
 gntdbccnma ndvntayc 18  
  
 <210> 22  
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 <223> oligonucleotide primer  
  
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 <222> (1)...(18)  
 <223> n = A,T,C or G  
  
 <400> 22  
 cnahvggnkt nhbnatrg 18  
  
 <210> 23  
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 tnhdnggnmr ntdbtgyg 18  
  
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<400> 24

andhncnky nahvacrc

18

<210> 25

<211> 24

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<223> oligonucleotide primer ZC21,119

<400> 25

aggacgatgg tgtggacaca agga

24

<210> 26

<211> 24

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<213> Artificial Sequence

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<223> oligonucleotide primer ZC21,987

<400> 27

caacctgttg ttgtcccg cacc

24

<210> 28

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC17,251

<400> 28

tctggacgtc ctctgctgg tatag

25

<210> 29

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC17,252

<400> 29

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25

<210> 30

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC17,156

<400> 30

gagtggcaac ttccagggcc aggagag

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<211> 27

<212> DNA

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<223> oligonucleotide primer ZC17,157



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 <210> 32  
 <211> 1760  
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 <221> CDS  
 <222> (154)...(1191)  
  
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 agtgcagcct tccccctggcg gtggtgaaag agactcggga gtcgctgctt ccaaagtgcc 120  
 cgccgtgagt gagctctcac cccagtcagc caa atg agc ctc ttc ggg ctt ctc 174  
 Met Ser Leu Phe Gly Leu Leu  
 1 5  
  
 ctg ctg aca tct gcc ctg gcc ggc cag aga cag ggg act cag gcg gaa 222  
 Leu Leu Thr Ser Ala Leu Ala Gly Gln Arg Gln Gly Thr Gln Ala Glu  
 10 15 20  
  
 tcc aac ctg agt agt aaa ttc cag ttt tcc agc aac aag gaa cag aac 270  
 Ser Asn Leu Ser Ser Lys Phe Gln Phe Ser Ser Asn Lys Glu Gln Asn  
 25 30 35  
  
 gga gta caa gat cct cag cat gag aga att att act gtg tct act aat 318  
 Gly Val Gln Asp Pro Gln His Glu Arg Ile Ile Thr Val Ser Thr Asn  
 40 45 50 55  
  
 gga agt att cac agc cca agg ttt cct cat act tat cca aga aat acg 366  
 Gly Ser Ile His Ser Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr  
 60 65 70  
  
 gtc ttg gta tgg aga tta gta gca gta gag gaa aat gta tgg ata caa 414  
 Val Leu Val Trp Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln  
 75 80 85  
  
 ctt acg ttt gat gaa aga ttt ggg ctt gaa gac cca gaa gat gac ata 462  
 Leu Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile  
 90 95 100

tgc aag tat gat ttt gta gaa gtt gag gaa ccc agt gat gga act ata	510
Cys Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile	
105 110 115	
tta ggg cgc tgg tgt ggt tct ggt act gta cca gga aaa cag att tct	558
Leu Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser	
120 125 130 135	
aaa gga aat caa att agg ata aga ttt gta tct gat gaa tat ttt cct	606
Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro	
140 145 150	
tct gaa cca ggg ttc tgc atc cac tac aac att gtc atg cca caa ttc	654
Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro Gln Phe	
155 160 165	
aca gaa gct gtg agt cct tca gtg cta ccc cct tca gct ttg cca ctg	702
Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala Leu Pro Leu	
170 175 180	
gac ctg ctt aat aat gct ata act gcc ttt agt acc ttg gaa gac ctt	750
Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr Leu Glu Asp Leu	
185 190 195	
att cga tat ctt gaa cca gag aga tgg cag ttg gac tta gaa gat cta	798
Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu Asp Leu Glu Asp Leu	
200 205 210 215	
tat agg cca act tgg caa ctt ctt ggc aag gct ttt gtt ttt gga aga	846
Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Val Phe Gly Arg	
220 225 230	
aaa tcc aga gtg gtg gat ctg aac ctt cta aca gag gag gta aga tta	894
Lys Ser Arg Val Val Asp Leu Asn Leu Leu Thr Glu Glu Val Arg Leu	
235 240 245	
tac agc tgc aca cct cgt aac ttc tca gtg tcc ata agg gaa gaa cta	942
Tyr Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu	
250 255 260	
aag aga acc gat acc att ttc tgg cca ggt tgt ctc ctg gtt aaa cgc	990
Lys Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg	
265 270 275	

tgt ggt ggg aac tgt gcc tgt tgt ctc cac aat tgc aat gaa tgt caa 1038  
 Cys Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln  
 280 285 290 295

tgt gtc cca agc aaa gtt act aaa aaa tac cac gag gtc ctt cag ttg 1086  
 Cys Val Pro Ser Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu  
 300 305 310

aga cca aag acc ggt gtc agg gga ttg cac aaa tca ctc acc gac gtg 1134  
 Arg Pro Lys Thr Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val  
 315 320 325

gcc ctg gag cac cat gag gag tgt gac tgt gtg tgc aga ggg agc aca 1182  
 Ala Leu Glu His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr  
 330 335 340

gga gga tag ccgcatcacc accagcagct cttgccaga gctgtgcagt 1231  
 Gly Gly \*  
 345

gcagtggctg attctattag agaacgtatg cgttatctcc atccttaatc tcagttgttt 1291  
 gcttcaagga cctttcatct tcaggattta cagtgcattc tgaagagga gacatcaaac 1351  
 agaattagga gttgtgcaac agctcttttg agaggaggcc taaaggacag gaaaaaggt 1411  
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 ggtaattgta gtacagaaaa aaaactgtgc aagtgagcac ctgattccgt tgccttgctt 1591  
 aactctaaag ctccatgtcc tgggcctaaa atcgtataaa atctggattt tttttttttt 1651  
 tttttgctca tattcacata tgtaaaccag aacattctat gtactacaaa cctgtgtttt 1711  
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<210> 33

<211> 345

<212> PRT

<213> Homo sapiens

<400> 33

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 20 25 30  
 Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln His Glu Arg  
 35 40 45

Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro Arg Phe Pro  
 50 55 60  
 His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu Val Ala Val  
 65 70 75 80  
 Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu  
 85 90 95  
 Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu  
 100 105 110  
 Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr  
 115 120 125  
 Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe  
 130 135 140  
 Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr  
 145 150 155 160  
 Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu  
 165 170 175  
 Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala  
 180 185 190  
 Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp  
 195 200 205  
 Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly  
 210 215 220  
 Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu  
 225 230 235 240  
 Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser  
 245 250 255  
 Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro  
 260 265 270  
 Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu  
 275 280 285  
 His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys  
 290 295 300  
 Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu  
 305 310 315 320  
 His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp  
 325 330 335  
 Cys Val Cys Arg Gly Ser Thr Gly Gly  
 340 345

&lt;210&gt; 34

&lt;211&gt; 3571

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1049)...(2086)

&lt;400&gt; 34

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ctcgccagc	acctgttgc	ccgccagctg	gccgccgcg	ccccccgcg	ccccccgcg	180
cgcccgccg	ccagcccg	gccccgcg	cgcccgctg	ggggaaagt	gagacgggga	240
ggggacaaga	gcgatactc	aggccagcca	ggccttcct	tagccgccc	tgcttagccg	300
ccacctctc	tcagccctg	gtcctgccct	gccttagggc	aggcatccga	gcgctcgca	360
ctccgagcg	cccaagctct	cccggcttc	cgcagcactt	cgccgggtacc	cgagggaaact	420
tcggtggcca	ccgactgcag	caaggaggag	gctccgcggt	ggatccgggc	cagtcccag	480
tcgtccccg	ggcctctctg	cccgccggg	accgcgcgg	cactcgcagg	gcacggtccc	540
ctccccccag	gtgggggtg	ggcgccgct	gccgcccca	tcagcagctt	tgctatgat	600
cccaaggtgc	tcgcctcgt	gccgacctg	cttcagctt	ggcttggcg	gaccccgagt	660
cctcgctgt	gtcctgtccc	ccaaactgac	agggtctccc	tcgagtcgc	cacgactcat	720
cgccgctccc	ccgcgtccc	acccttctt	tcctccctg	cctaccccca	ccccccgcac	780
ttcgccacag	ctcaggattt	gtttaaact	tgggaaactg	gttcaggctc	agggtttgct	840
ttgatcctt	tcaaaaactg	gagacacaga	agagggctct	agggaaaaact	tttggatggg	900
attatgtgga	aactaccctg	cgattctctg	ctgccagagc	cgcccgaggc	cttccaccgc	960
agcgcagcct	ttccccggct	gggctgagcc	ttggagtcgt	cgcttcccca	gtgcccgccg	1020
cgagtgagcc	ctcgccccag	tcagccaa	atg ctc ctc ctc	ggc ctc ctc ctg		1072

Met Leu Leu Leu Gly Leu Leu Leu

1

5

ctg aca tct gcc	ctg gcc ggc	caa aga acg	ggg act	cgg gct	gag tcc	1120
Leu Thr Ser Ala	Leu Ala Gly Gln	Arg Thr Gly Thr	Arg Ala Glu	Ser		
10	15	20				

aac ctg agc agc	aag ttg	cag ctc tcc	agc gac	aag gaa	cag aac	gga	1168
Asn Leu Ser Ser	Lys Leu	Ser Ser Asp	Lys Glu	Gln Asn	Gly		
25	30	35			40		

gtg caa gat ccc	cgg cat	gag aga gtt	gtc act	ata tct	ggt aat	ggg	1216
Val Gln Asp Pro	Arg His	Glu Arg Val	Val Thr	Ile Ser	Gly Asn	Gly	
	45	50			55		

agc atc cac agc	ccg aag	ttt cct	cat aca	tac cca	aga aat	atg gtg	1264
Ser Ile His Ser	Pro Lys	Phe Pro	His Thr	Tyr Pro	Arg Asn	Met Val	
60		65			70		

ctg gtg tgg aga tta gtt gca gta gat gaa aat gtg cgg atc cag ctg Leu Val Trp Arg Leu Val Ala Val Asp Glu Asn Val Arg Ile Gln Leu 75 80 85	1312
aca ttt gat gag aga ttt ggg ctg gaa gat cca gaa gac gat ata tgc Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys 90 95 100	1360
aag tat gat ttt gta gaa gtt gag gag ccc agt gat gga agt gtt tta Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Ser Val Leu 105 110 115 120	1408
gga cgc tgg tgt ggt tct ggg act gtg cca gga aag cag act tct aaa Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Thr Ser Lys 125 130 135	1456
gga aat cat atc agg ata aga ttt gta tct gat gag tat ttt cca tct Gly Asn His Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro Ser 140 145 150	1504
gaa ccc gga ttc tgc atc cac tac agt att atc atg cca caa gtc aca Glu Pro Gly Phe Cys Ile His Tyr Ser Ile Ile Met Pro Gln Val Thr 155 160 165	1552
gaa acc acg agt cct tcg gtg ttg ccc cct tca tct ttg tca ttg gac Glu Thr Thr Ser Pro Ser Val Leu Pro Pro Ser Ser Leu Ser Leu Asp 170 175 180	1600
ctg ctc aac aat gct gtg act gcc ttc agt acc ttg gaa gag ctg att Leu Leu Asn Asn Ala Val Thr Ala Phe Ser Thr Leu Glu Glu Leu Ile 185 190 195 200	1648
cgg tac cta gag cca gat cga tgg cag gtg gac ttg gac agc ctc tac Arg Tyr Leu Glu Pro Asp Arg Trp Gln Val Asp Leu Asp Ser Leu Tyr 205 210 215	1696
aag cca aca tgg cag ctt ttg ggc aag gct ttc ctg tat ggg aaa aaa Lys Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Leu Tyr Gly Lys Lys 220 225 230	1744
agc aaa gtg gtg aat ctg aat ctc ctc aag gaa gag gta aaa ctc tac Ser Lys Val Val Asn Leu Asn Leu Leu Lys Glu Glu Val Lys Leu Tyr 235 240 245	1792

agc tgc aca ccc cgg aac ttc tca gtg tcc ata cgg gaa gag cta aag	1840
Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu Lys	
250 255 260	
agg aca gat acc ata ttc tgg cca ggt tgt ctc ctg gtc aag cgc tgt	1888
Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg Cys	
265 270 275 280	
gga gga aat tgt gcc tgt tgt ctc cat aat tgc aat gaa tgt cag tgt	1936
Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys	
285 290 295	
gtc cca cgt aaa gtt aca aaa aag tac cat gag gtc ctt cag ttg aga	1984
Val Pro Arg Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg	
300 305 310	
cca aaa act gga gtc aag gga ttg cat aag tca ctc act gat gtg gct	2032
Pro Lys Thr Gly Val Lys Gly Leu His Lys Ser Leu Thr Asp Val Ala	
315 320 325	
ctg gaa cac cac gag gaa tgt gac tgt gtg tgt aga gga aac gca gga	2080
Leu Glu His His Glu Glu Cys Asp Cys Val Cys Arg Gly Asn Ala Gly	
330 335 340	
ggg taa ctgcagcctt cgtacgagca cacgtgagca ctggcattct gtgtaccccc	2136
Gly *	
345	
acaagcaacc ttcattccca ccagcgttgg ccgcagggct ctcagctgct gatgctggct	2196
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gcactgcctt ctgaggaagc ccagacaat ggtcttctga ccacagaaac aaatgaaatg	2376
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cacttgattg tgaacaatgc agaataactt ggatttctcc aacctgtttg catagataga	2556
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ttggaggaaa ggtgcggtca tggtttgag aaagcacacc tgcacagagg agtggccttc	2736
ccttcacctc cctctgaggt gccttctgtg ttctattgtg tatattttta tattctcctt	2796
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atttaattatt ctttttttag acaacctaga gcaattattt ttgacttgat aatttttttt	2916
tctaacaaca attgttatag ccagaagaac aaagatgatt gatataaaaa tctgttgct	2976

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ctgacaaaa catatgtatt tcttccttgt atggtgctag agcttagcgt catctgcatt 3036
tgaaaagatg gaatggggaa gtttttagaa ttggtaggtc gcagggacag tttgataaca 3096
actgtactat catcaattcc caattctgtt cttagagcta cgaacagaac agagcttgag 3156
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aagcacgtcc ccagaaacct cgaccatttc taggcacagt gttctgggct atgctgcgct 3276
gtatggacat atcctattta ttccaatact aggggtttat tacctttaaa ctctgtctcca 3336
tacacttgta ttaatacatg gatattttta tgtacagaag tatatcattt aaggagttca 3396
cttattatac tctttggcaa ttgcaaagaa aatcaacata atacattgct tgtaaatgct 3456
taatctgtgc ccaagttttg tggtgactat ttgaattaaa atgtattgaa tcatacaata 3516
aaataatctg gctatttttg ggaaaaaaaa aaaaaaaaaa aaaaaggcg gccgc 3571

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&lt;210&gt; 35

&lt;211&gt; 345

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 35

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Met Leu Leu Leu Gly Leu Leu Leu Thr Ser Ala Leu Ala Gly Gln
  1             5             10             15
Arg Thr Gly Thr Arg Ala Glu Ser Asn Leu Ser Ser Lys Leu Gln Leu
      20             25             30
Ser Ser Asp Lys Glu Gln Asn Gly Val Gln Asp Pro Arg His Glu Arg
      35             40             45
Val Val Thr Ile Ser Gly Asn Gly Ser Ile His Ser Pro Lys Phe Pro
      50             55             60
His Thr Tyr Pro Arg Asn Met Val Leu Val Trp Arg Leu Val Ala Val
      65             70             75             80
Asp Glu Asn Val Arg Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
      85             90             95
Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
      100            105            110
Glu Pro Ser Asp Gly Ser Val Leu Gly Arg Trp Cys Gly Ser Gly Thr
      115            120            125
Val Pro Gly Lys Gln Thr Ser Lys Gly Asn His Ile Arg Ile Arg Phe
      130            135            140
Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
      145            150            155            160
Ser Ile Ile Met Pro Gln Val Thr Glu Thr Thr Ser Pro Ser Val Leu
      165            170            175
Pro Pro Ser Ser Leu Ser Leu Asp Leu Leu Asn Asn Ala Val Thr Ala
      180            185            190
Phe Ser Thr Leu Glu Glu Leu Ile Arg Tyr Leu Glu Pro Asp Arg Trp
      195            200            205

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Gln Val Asp Leu Asp Ser Leu Tyr Lys Pro Thr Trp Gln Leu Leu Gly  
 210 215 220  
 Lys Ala Phe Leu Tyr Gly Lys Lys Ser Lys Val Val Asn Leu Asn Leu  
 225 230 235 240  
 Leu Lys Glu Glu Val Lys Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser  
 245 250 255  
 Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro  
 260 265 270  
 Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu  
 275 280 285  
 His Asn Cys Asn Glu Cys Gln Cys Val Pro Arg Lys Val Thr Lys Lys  
 290 295 300  
 Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Lys Gly Leu  
 305 310 315 320  
 His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp  
 325 330 335  
 Cys Val Cys Arg Gly Asn Ala Gly Gly  
 340 345

&lt;210&gt; 36

&lt;211&gt; 600

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (496)...(592)

&lt;400&gt; 36

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gcctctcagg	ggccgcggcc	ggggctggag	aacgctgctg	ctccgctcgc	ctgccccgct	180
agattcggcg	ctgccccgcc	cctgcagcct	gtgtgcagc	tgccggccac	cggagggggc	240
gaacaaacaa	acgtcaacct	gttgttgtc	ccgtcaccat	ttatcagctc	agcaccacaa	300
ggaagtgcgg	caccacacg	cgctcgaaaa	gttcagcatg	caggaagttt	ggggagagct	360
cggcgattag	cacagcgacc	cgggccagcg	cagggcgagc	gcagacggcg	agagcgcagg	420
gcggcgcggc	gtcggtcgcc	ggagcagaac	ccggcttttt	cttgagcgga	cgctgtctct	480
agtgcgtgat	cccaa atg	cac cgg ctc	atc ttt gtc	tac act cta	atc tgc	531
	Met	His	Arg	Leu	Ile Phe Val Tyr Thr Leu Ile Cys	
	1		5		10	

tcc atc aaa gct t gagtatttc 600  
Ser Ile Lys Ala  
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<210> 38  
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<212> DNA  
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<223> oligonucleotide primer ZC22,686

<210> 39  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> peptide

<400> 39  
Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln  
1 5 10 15  
Ile Lys

<210> 40  
 <211> 25  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> peptide

<400> 40  
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 1 5 10 15  
 Tyr Arg Gly Arg Ser Tyr His Asp Cys  
 20 25

<210> 41  
 <211> 24  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> peptide

<400> 41  
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 Ala Leu Val Asp Ile Gln Leu Asp  
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<210> 42  
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<220>  
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<210> 43

<211> 42  
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<400> 43  
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<210> 44  
 <211> 36  
 <212> DNA  
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<220>  
 <223> oligonucleotide primer ZC26137

<400> 44  
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<210> 45  
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<210> 46  
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 <212> DNA  
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<210> 47  
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<210> 48  
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<220>  
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<210> 49  
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<220>  
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<220>  
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<210> 51  
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 <212> DNA  
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<220>  
 <223> oligonucleotide primer ZC14063

<400> 51  
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<210> 52  
 <211> 1472  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (93)...(1205)

<400> 52  
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 Met Gln Arg Leu Val Leu Val  
 1 5  
 tcc att ctc ctg tgc gcg aac ttt agc tgc tat ccg gac act ttt gcg 161  
 Ser Ile Leu Leu Cys Ala Asn Phe Ser Cys Tyr Pro Asp Thr Phe Ala  
 10 15 20  
 act ccg cag aga gca tcc atc aaa gct ttg cgc aat gcc aac ctc agg 209  
 Thr Pro Gln Arg Ala Ser Ile Lys Ala Leu Arg Asn Ala Asn Leu Arg  
 25 30 35  
 aga gat gag agc aat cac ctc aca gac ttg tac cag aga gag gag aac 257  
 Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Gln Arg Glu Glu Asn  
 40 45 50 55  
 att cag gtg aca agc aat ggc cat gtg cag agt cct cgc ttc ccg aac 305  
 Ile Gln Val Thr Ser Asn Gly His Val Gln Ser Pro Arg Phe Pro Asn  
 60 65 70

agc tac cca agg aac ctg ctt ctg aca tgg tgg ctc cgt tcc cag gag 353  
 Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Trp Leu Arg Ser Gln Glu  
 75 80 85

aaa aca cgg ata caa ctg tcc ttt gac cat caa ttc gga cta gag gaa 401  
 Lys Thr Arg Ile Gln Leu Ser Phe Asp His Gln Phe Gly Leu Glu Glu  
 90 95 100

gca gaa aat gac att tgt agg tat gac ttt gtg gaa gtt gaa gaa gtc 449  
 Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Val Glu Glu Val  
 105 110 115

tca gag agc agc act gtt gtc aga gga aga tgg tgt ggc cac aag gag 497  
 Ser Glu Ser Ser Thr Val Val Arg Gly Arg Trp Cys Gly His Lys Glu  
 120 125 130 135

atc cct cca agg ata acg tca aga aca aac cag att aaa atc aca ttt 545  
 Ile Pro Pro Arg Ile Thr Ser Arg Thr Asn Gln Ile Lys Ile Thr Phe  
 140 145 150

aag tct gat gac tac ttt gtg gca aaa cct gga ttc aag att tat tat 593  
 Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys Ile Tyr Tyr  
 155 160 165

tca ttt gtg gaa gat ttc caa ccg gaa gca gcc tca gag acc aac tgg 641  
 Ser Phe Val Glu Asp Phe Gln Pro Glu Ala Ala Ser Glu Thr Asn Trp  
 170 175 180

gaa tca gtc aca agc tct ttc tct ggg gtg tcc tat cac tct cca tca 689  
 Glu Ser Val Thr Ser Ser Phe Ser Gly Val Ser Tyr His Ser Pro Ser  
 185 190 195

ata acg gac ccc act ctc act gct gat gcc ctg gac aaa act gtc gca 737  
 Ile Thr Asp Pro Thr Leu Thr Ala Asp Ala Leu Asp Lys Thr Val Ala  
 200 205 210 215

gaa ttc gat acc gtg gaa gat cta ctt aag cac ttc aat cca gtg tct 785  
 Glu Phe Asp Thr Val Glu Asp Leu Leu Lys His Phe Asn Pro Val Ser  
 220 225 230

tgg caa gat gat ctg gag aat ttg tat ctg gac acc cct cat tat aga 833  
 Trp Gln Asp Asp Leu Glu Asn Leu Tyr Leu Asp Thr Pro His Tyr Arg  
 235 240 245

ggc agg tca tac cat gat cgg aag tcc aaa gtg gac ctg gac agg ctc 881  
 Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu Asp Arg Leu  
 250 255 260

aat gat gat gtc aag cgt tac agt tgc act ccc agg aat cac tct gtg 929  
 Asn Asp Asp Val Lys Arg Tyr Ser Cys Thr Pro Arg Asn His Ser Val  
 265 270 275

aac ctc agg gag gag ctg aag ctg acc aat gca gtc ttc ttc cca cga 977  
 Asn Leu Arg Glu Glu Leu Lys Leu Thr Asn Ala Val Phe Phe Pro Arg  
 280 285 290 295

tgc ctc ctc gtg cag cgc tgt ggt ggc aac tgt ggt tgc gga act gtc 1025  
 Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys Gly Thr Val  
 300 305 310

aac tgg aag tcc tgc aca tgc agc tca ggg aag aca gtg aag aag tat 1073  
 Asn Trp Lys Ser Cys Thr Cys Ser Ser Gly Lys Thr Val Lys Lys Tyr  
 315 320 325

cat gag gta ttg aag ttt gag cct gga cat ttc aag aga agg ggc aaa 1121  
 His Glu Val Leu Lys Phe Glu Pro Gly His Phe Lys Arg Arg Gly Lys  
 330 335 340

gct aag aat atg gct ctt gtt gat atc cag ctg gat cat cat gag cga 1169  
 Ala Lys Asn Met Ala Leu Val Asp Ile Gln Leu Asp His His Glu Arg  
 345 350 355

tgt gac tgt atc tgc agc tca aga cca cct cga taa aacactatgc 1215  
 Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg \*  
 360 365 370

acatctgtac ttgattatg aaaggacctt taggttacaa aaaccctaag aagcttctaa 1275  
 tctcagtga atgaatgcat atggaatgt tgctttgtta gtgccatggc aagaagaagc 1335  
 aaatatcatt aatttctata tacataaaca taggaattca cttatcaata gtagtgaag 1395  
 atatgtatat atacttatat acatgactag ctctatgtat gtaaatagat taaatacttt 1455  
 attcagtata ttactgt 1472

&lt;210&gt; 53

&lt;211&gt; 370

&lt;212&gt; PRT

&lt;213&gt; Mus musculus



&lt;400&gt; 53

Met Gln Arg Leu Val Leu Val Ser Ile Leu Leu Cys Ala Asn Phe Ser  
 1 5 10 15  
 Cys Tyr Pro Asp Thr Phe Ala Thr Pro Gln Arg Ala Ser Ile Lys Ala  
 20 25 30  
 Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp  
 35 40 45  
 Leu Tyr Gln Arg Glu Glu Asn Ile Gln Val Thr Ser Asn Gly His Val  
 50 55 60  
 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr  
 65 70 75 80  
 Trp Trp Leu Arg Ser Gln Glu Lys Thr Arg Ile Gln Leu Ser Phe Asp  
 85 90 95  
 His Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp  
 100 105 110  
 Phe Val Glu Val Glu Glu Val Ser Glu Ser Ser Thr Val Val Arg Gly  
 115 120 125  
 Arg Trp Cys Gly His Lys Glu Ile Pro Pro Arg Ile Thr Ser Arg Thr  
 130 135 140  
 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys  
 145 150 155 160  
 Pro Gly Phe Lys Ile Tyr Tyr Ser Phe Val Glu Asp Phe Gln Pro Glu  
 165 170 175  
 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Phe Ser Gly  
 180 185 190  
 Val Ser Tyr His Ser Pro Ser Ile Thr Asp Pro Thr Leu Thr Ala Asp  
 195 200 205  
 Ala Leu Asp Lys Thr Val Ala Glu Phe Asp Thr Val Glu Asp Leu Leu  
 210 215 220  
 Lys His Phe Asn Pro Val Ser Trp Gln Asp Asp Leu Glu Asn Leu Tyr  
 225 230 235 240  
 Leu Asp Thr Pro His Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser  
 245 250 255  
 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Val Lys Arg Tyr Ser Cys  
 260 265 270  
 Thr Pro Arg Asn His Ser Val Asn Leu Arg Glu Glu Leu Lys Leu Thr  
 275 280 285  
 Asn Ala Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly  
 290 295 300  
 Asn Cys Gly Cys Gly Thr Val Asn Trp Lys Ser Cys Thr Cys Ser Ser  
 305 310 315 320

Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Lys Phe Glu Pro Gly  
325 330 335  
His Phe Lys Arg Arg Gly Lys Ala Lys Asn Met Ala Leu Val Asp Ile  
340 345 350  
Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro  
355 360 365  
Pro Arg  
370